

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS:

1. (currently amended) A method for predicting an increased risk for onset of open angle glaucoma in a human subject, comprising the steps of:

(a) assaying a polynucleotide sample from a human subject for the presence of at least one nucleotide mutation of at least one nucleotide in the coding region of the an optineurin (OPTN) gene of set forth in SEQ ID NO:1, wherein said nucleotide mutation is selected from the group consisting of a mutation at position 619 of SEQ ID NO:1 and a mutation at position 898 of SEQ ID NO:1; and

(b) predicting an said subject, wherein when said mutation is present, said subject is predicted to have an increased risk for onset of open angle glaucoma in said human subject when at least one of said nucleotide mutations is present.

2. (currently amended) The method according to of claim 1, wherein the mutation at position 619 is a substitution of G for A coding region of an OPTN gene comprises nucleotides 1 to 1734 of SEQ ID NO:1.

3. (currently amended) The method according to of claim 12, wherein the said mutation is a substitution of G for A at position 619 or a substitution of A for G at position 898 is a substitution of A for G, or both, in SEQ ID NO:1.

4. (currently amended) The method according to of claim 12, wherein the presence of the mutation at position 619 is assayed by performing nucleic acid amplification on a polynucleotide sample obtained from said human subject using at least one oligonucleotide primer pair selected from the group consisting of:

(a) an oligonucleotide primer pair consisting of the nucleotide sequences of SEQ ID NOS:21 and 22; and

(b) an oligonucleotide primer pair wherein each member of the primer pair is a complement of one member of the oligonucleotide primer pair of (a)said mutation is a deletion of one or more nucleotides in SEQ ID NO: 1.

5. (currently amended) The method according to or claim 12, wherein the presence of the mutation at position 898 is assayed by performing nucleic acid amplification on a polynucleotide sample obtained from said human subject using at least one oligonucleotide primer pair selected from the group consisting of:

(a) an oligonucleotide primer pair consisting of the nucleotide sequences of SEQ ID NOs:27 and 28; and

(b) an oligonucleotide primer pair wherein each member of the primer pair is a complement of one member of the oligonucleotide primer of (a)said mutation is an insertion of one or more nucleotides in SEQ ID NO: 1.

6-13. (canceled).